Supplementary Materials

Selection of Studies

The BrainMap database was employed for the retrieval of relevant neuroimaging experiments. As reported in the User Manual, BrainMap uses a structured standardized coding scheme which describes published human neuroimaging experimental results. This taxonomy has been used to describe over 3600 publications and 15000 experiments, drawing upon over 110000 subjects and reporting over 120000 coordinates. The main division of the coding scheme is between *structural* (VBM) and *functional* data. For this meta-analysis only papers labeled as "Structural" have been used. Considering the studies in this category, the database consists of 980 papers, 3093 experiments, 73938 subjects and 21481 locations.

The software application "Sleuth" has been used to search the database for experiments of interest and view the relevant search results in a standard brain space. This procedure allowed us to identify 242 studies involving SCZD, ASD, and OCSD (126, 96 and 20, respectively).

In a second step, a systematic search strategy was used to identify relevant studies whose temporal boundaries are not included in the BrainMap database, published until 15 July 2016, across the online database most frequently used in the international literature (Medline database with PubMed literature search: http://www.ncbi.nlm.nih.gov/pubmed) involving SCZD, ASD, and OCSD as they are defined by DSM-5 (American Psychiatric Association, 2013).

First, association measures have been analyzed to get a perspective on the biomedical research literature: co-occurrences of all the terms concerning psychiatric spectra and neuroimaging acquisition technique have been analyzed by measuring the degree to which two queries coincide among all publications. The corresponding co-occurrences of publications have been returned in the form of natural logarithm of the Jaccard index (ln J) (Jaccard, 1901). Secondly, we have adopted the MeSH hierarchy for Mental Disorders in PubMed automatic routines to find relevant published article concerning ASD, SCZD and OCSD. In particular, we provided a *set* of PubMed queries as input, adopting Boolean operators and PubMed search field tags. Indeed, to identify the greatest number of items we used the function [ALL] concerning the possibility to find MeSH terms in "all field" of an article. For each spectrum, the search algorithm has been constructed as follows:

• FIRST SET

o (#spectrum 1: "autism spectrum disorder" OR [ALL] "ASD" [ALL]) AND (# acquisition technique: "voxel-based morphometry" [ALL] OR "VBM" [ALL]; "diffusion tensor imaging" OR "DTI" [ALL]).

• SECOND SET

o (#spectrum 2: "obsessive-compulsive disorder" OR [ALL] "OCD" [ALL]) AND (# acquisition technique: "voxel-based morphometry" [ALL] OR "VBM" [ALL]; "diffusion tensor imaging" OR "DTI" [ALL]).

• THIRD SET

o (#spectrum 3: "schizophrenia" OR [ALL] "schizoaffective disorder" [ALL]) AND (# acquisition technique: "voxel-based morphometry" [ALL] OR "VBM" [ALL]; "diffusion tensor imaging" OR "DTI" [ALL]).

As regards the search and selection process, additional considerations are necessary: (1) concerning the OCSD, PubMed has found under the heading of the spectrum also articles about Tic disorder that, after a manual verification, were found to contain the correct MeSH term of classification [i.e., Study ID: 12,13,31,50,51,71]; (2) at the beginning of the data collection in 2012, PubMed did not contain a MeSH term for SCZD: so it has been necessary to resort to the terms "schizophrenia" and "schizoaffective disorder".

Up until 15 July 2016, 1419 papers involving SCZD, ASD, and OCSD had been indexed on BrainMap database and PubMed. All the selected articles that did not meet the inclusion criteria were excluded. In particular, two experienced researchers have reviewed all the articles using a double-blind procedure to ensure: (1) both the presence of the healthy control group and the pathological sample; (2) that the results were reported by using the Talairach/Tournoux or Montreal Neurological Institute (MNI) coordinates; (3) that the foci of interest had a significance of at least ≤ 0.05 ; (4) that the studies described cerebral structural changes visible with VBM or DTI (only FA technique); (5) that the studies were original works; (6) that original diagnosis was made on the basis of DSM criteria and clinical test batteries. Furthermore, instances of multiple references to the same datasets across articles were identified so as to make sure that only one reference to the same data contributed to the coordinates for the present meta-analysis (See Graph S1 [PRISMA flow chart] and Table S1).

All the studies were examined independently to detect dissimilarities or discrepancies, which were afterward collectively discussed and resolved. The researchers who carried out this research stage have reached substantial agreement (% of agreement = 94.3096 ; Cohen's K= 0.7409).

Relevant descriptive information was extracted from each article. On the grounds of the aforementioned criteria, 203 papers were included in the meta-analysis, with 218 identified experimental samples and a total of 8693 subjects: 1719 individuals of the ASD group, 1738 of the OCSD group, and 5236 of the SCZD group. Tables S1-S2 provide a detailed description of methods and the sample of the selected studies (see also Figure S2). The number of WM and GM changes foci were established for each study. In order to facilitate analysis, coordinates from MNI space were converted into Talairach coordinates by using Lancaster transformation (Lancaster et al., 2007).

Supplementary Tables and Figures

Table S1. Selected studies for the meta-analysis 1 .

¹ The items shown in the table are the result of the entire selection process as shown in PRISMA (2009) flow chart and table S2. The starting point for the selection can be traced in the algorithms and in the additional considerations previously proposed.

* The average age (standard deviation) or age range is reported on the basis of what is specified by the authors.

** Where no information was provided, the voxel-size was expressed.

Table S2. Description of the total experimental sample with the respective diagnostic labeling.

* Diagnoses are reported on the basis of what is specified by the authors.

** Values have been calculated on the basis of the studies bearing the required information.

ASD = Autism Spectrum Disorder

OCSD = Obsessive Compulsive Spectrum Disorder

SCZD = Schizophrenia Spectrum Disorder

 $N =$ number of subjects from each diagnostic category

Legend

SCZD SCHZ = Schizophrenia Simplex; SCZD PAR SCHZ = Paranoia with Schizophrenia symptoms; SCZD FEP SCHZ = First Episode Schizophrenia; SCZD EOS = Early Onset Symptoms of Psychosis; SCZD HALL = Hallucination; SCZD Aud Hall = Auditory Hallucination; SCZD FEP = First Episode Psychosis; SCZD MIXED = Mixed form; SCZD ACUTE NO HALL = Acute Psychosis with no hallucination; SCZD PAR = paranoia; OCSD TOU = Tourette Syndrome; OCSD OCD = Obsessive-Compulsive Disorder; OCSD TRI = Trichotillomania; ASD_MIXED = Mixed form; ASD_PA = Primary Autism; ASD_HFA = Highfunctionality; ASD_ASP = Asperger; ASD_PDD = Pervasive Development Disorder.

Table S4². Gray matter (GM) and white matter (WM) variations with relative numbers of foci for each of the selected psychiatric spectra.

 2^2 The items shown in the table are the result of the entire selection process as shown in PRISMA (2009) flow chart and table S2. The starting point for the selection can be traced in the algorithms and in the additional considerations previously proposed.

The insular nodes and their resting state functional connectivity

Subjects and image acquisition

For the anatomical covariance and functional connectivity measures we used the Beijing dataset which has been publicly released within the "1000 Functional Connectomes" Project. This dataset consists of 198 subjects (76 males and 122 female) with age ranging from 18 to 26 years, mean 21.16, SD 1.83, that underwent structural and resting state scans. All subjects were right-handed and had no history of neurological or psychiatric disorders. Written informed consent was obtained from each participant, and the study was approved by the Institutional Review Board of Beijing Normal University Imaging Center for Brain Research.

MRI data were acquired using a SIEMENS TRIO 3-Tesla scanner in the Beijing Normal University Imaging Center for Brain Research. Participants lay supine with their head fixed by straps and foam pads so as to minimize movements. During the resting-state session, participants were instructed to be as still as possible and let their mind roam. Functional images were obtained using an EPI sequence with the following parameters: 33 axial slices, thickness/gap = 3/0.6 mm, inplane resolution = 64×64 , TR = 2000 ms, TE = 30 ms, flip angle = 90° , FOV = 200×200 mm. Furthermore, a T1-weighted sagittal three-dimensional magnetization-prepared rapid gradient echo (MPRAGE) sequence was acquired, which covered the entire brain: 128 slices, $TR = 2530$ ms, TE $= 3.39$ ms, slice thickness = 1.33 mm, flip angle = 7°, inversion time = 1100 ms, FOV = 256 mm \times 256 mm, and in-plane resolution = 256×192 .

Preprocessing

In order to analyze the functional connectivity of the insula we used the DPABI processing tool rel. 2.3 (Yan, et al., 2016). All the preprocessing was performed by employing the advanced DPARSF module V3.2. The first 10 volumes of the functional images are often discarded both for achieving signal equilibrium and for letting participants adapt to the scanning noise. All volume slices were corrected for different signal acquisition times taking the middle slice as reference and using the odd slice order. Then, the images' time series of every subject were realigned. After the realignment, individual structural images were co-registered to the mean functional image. The transformed structural images were then segmented into GM, WM and CSF. To remove the nuisance signals, we employed the Friston 24-parameter model (Friston, et al., 1996), three translation and three rotation parameters of the current volume and the preceding volume, plus each of these values squared, so as to regress out head motion effects from the realigned data. The signals from both WM and CSF were regressed out to reduce respiratory and cardiac effects. In addition, linear and quadratic trends were also included as regressors, since the BOLD signal exhibits low-frequency drifts. The DARTEL tool was used to transform the functional data from individual native space to MNI space. Spatial smoothing (FWMH kernel: 4.5 mm) was applied to the functional images and temporal filtering (0.01–0.1 Hz) was then performed on the time series. Finally, for every subject the mean time course of every insular ROI was extracted and correlated voxel-wise to all the voxels of the brain. These results were then summarized using a one sample t test. All the calculations were thresholded at a p<0.05 cluster-level, corrected for multiple comparison using the FSL randomize tool.

Clustering and visualization of alteration patterns

Clustering

To test if data can be decomposed in two or more groups we employed a clustering approach: the kmeans technique. This technique is an unsupervised learning algorithm that subdivides a set of objects in k groups according to their attributes. There are different types and methods of clustering in literature: we chose k-means because, compared to other algorithms, its runtime and performance are usually more efficient as the number of records increases (Bishop, 2006). Furthermore, since clusters are non-hierarchical, they do not overlap, which is important in our case, as we were looking for a clear partition between the three psychiatric spectra (Bishop, 2006; Thirion, et al., 2014).

For the k-means clustering we used an nxp matrix, in which rows correspond to points and columns to variables (attributes). We used as attributes the MA maps and as points the voxels. The optimal number of groups (k) was determined by the silhouette plot introduced by Kaufman and Rousseeuw (1990). The results of the silhouette plot showed that 2 was the best number of clusters calculated by this algorithm (Fig. S3).

In this study we applied both clustering and classification methods to analyze our data. The rationales for using the clustering technique as well as the machine learning method are different. We used the clustering technique to check if a "natural" decomposition of the voxels could emerge from each different psychiatric disorder. This allowed us to see whether or not there were interesting anatomical partitions that could differentiate ASD, SCZD, and OCSD.

Multidimensional scaling

To evaluate the similarity between the three different spectra of psychiatric disorders (represented by MA maps generated by the different experiments analyzed in this study) we used the multidimensional scaling (MDS) method. MDS mainly consists of data proximity analysis techniques to check hidden structures. For each paper, every MA map was transformed into a series of vectors containing all the values of the original matrix. Then a representational similarity matrix was constructed by computing the correlation *r* among all vectors. Vectors are constituted by the statistical values of the voxels pertaining to the MA maps. The distance matrix (or representational dissimilarity matrix) defined as $1 - r$ (Cauda, et al., 2014; Kriegeskorte, et al., 2008) was similarly created. The distance matrix was subjected to the multidimensional scaling analysis so as to obtain a geometrical representation of data deviation.

We evaluated the similarity by examining visually the MDS graphs, in which the multidimensional similarity/dissimilarity between pathology-derived MA maps are represented as 2D distances (expressed in arbitrary values). Similar pairs are placed close together and dissimilar pairs are placed far between each other (Fig. S3).

Figure S3. Left panel: Clustered gray matter (GM) distance matrices of the modeled activation (MA) maps relative to each of the examined experiments. Right panel: multidimensional scaling (MDS) of the modeled activation (MA) maps relative to each of the examined experiments (graphs

expressed in arbitrary units). In MDS graphs the multidimensional similarity/dissimilarity between pathology-derived MA maps are represented as 2D distances (expressed in arbitrary values). Similar pairs are placed close together and dissimilar pairs are placed far between each other.

Figure S4. Patel's k values for the 70 co-atrophy edges.

Schizophrenia vs the whole dataset

The results obtained with the analysis of schizophrenia data only are very similar to those obtained with the analysis of the whole dataset, in which all the three spectra are taken into consideration (Fig. S5-S6). Changes regard in particular Patel's k values of single edges, but the two networks are substantially very similar. These results are consistent with those illustrated in Figure S3, which shows that the first cluster (encompassing all the three spectra) represents the most part of our data.

Figure S5. Results of the morphometric co-atrophy network constructed with schizophrenia data only or with the whole dataset. Colors from blue to red indicate increasing Patel's k values (i.e., increasing co-alteration probabilities).

Figure S6. Results of the morphometric co-atrophy network constructed with schizophrenia data only or with the whole dataset. The left panel shows the differences between the results. Red edges are specific to schizophrenia, while green edges are specific to all the three spectra. The right panel shows the edges clustered by spatial distance. White lines indicate absence of edges, blue line their presence.

Figure S7. Relationship between experiments and edges in the Schizophrenia dataset. The figure illustrates how the results of the statistical analysis change if 10 experiments are removed from the SCZD sample at each simulation. With this procedure we were able to evaluate the variation of the number of significant edges estimated by our statistics. It is clear that the amount of edges decreases after every removal: after 50 experiments the number of significant edges collapses and after 40 experiments no edge can be identified.

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